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SEQUENCE LISTING

<110> HOOD, John
ELICEIRI, Brian
CHERESH, David

<120> METHODS AND COMPOSITIONS USEFUL FOR
MODULATION OF ANGIOGENESIS USING TYROSINE KINASE RAF AND RAS

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<141> 2000-08-11

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<151> 1999-08-13

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<151> 2000-07-05

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Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro
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aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc 267
Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly
35 40 45

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Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu
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ccg aac aag caa aga aca gtc aat gtg cga aat gga atg agc ttg 363
Pro Asn Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu
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His Asp Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu
80 85 90

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Cys Cys Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala
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Arg Leu Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu
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Gln Val Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala
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Leu Leu Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu
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His Cys Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile
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Arg Gln Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val
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cca gca cta cct tct ttg act atg cgt cgt atg cga gag tct gtt tcc 795
Pro Ala Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser
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agg atg cct gtt agt tct cag cac aga tat tct aca cct cac gcc ttc 843
Arg Met Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe
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acc ttt aac acc tcc agt ccc tca tct gaa ggt tcc ctc tcc cag agg 891
Thr Phe Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg
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cag agg tcg aca tcc aca cct aat gtc cac atg gtc agc acc acg ctg 939
Gln Arg Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu
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cag aga gat tca agc tat tat tgg gaa ata gaa gcc agt gaa gtg atg Gln Arg Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met 335 340 345 350	1179
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gac aac ctg gca att gtg acc cag tgg tgc gag ggc agc agc ctc tac Asp Asn Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr 415 420 425 430	1419
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aac atc atc cat aga gac atg aaa tcc aac aat ata ttt ctc cat gaa Asn Ile Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu 465 470 475	1563
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 Phe Met Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr
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 Lys Val Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile
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 gag ctg ctc caa cac tct cta ccg aag atc aac cgg agc gct tcc gag 1995
 Glu Leu Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu
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 Pro Ser Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr
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 ctg acc acg tcc ccg agg ctg cct gtc ttc tagttgactt tgcacccgtc 2093
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Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
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Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
65 70 75 80
Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
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Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
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Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
130 135 140
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
145 150 155 160
Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
165 170 175
Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
180 185 190
Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
195 200 205
Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
210 215 220
Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
225 230 235 240
Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
245 250 255
Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
260 265 270
Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
275 280 285
Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
290 295 300
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305 310 315 320
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg

1
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Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
355 360 365
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
370 375 380
Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
385 390 395 400
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
405 410 415
Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
420 425 430
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
435 440 445
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
450 455 460
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
465 470 475 480
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
485 490 495
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
500 505 510
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
515 520 525
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
530 535 540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
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Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
565 570 575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
580 585 590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
595 600 605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
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Thr Ser Pro Arg Leu Pro Val Phe
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gac ccc act ata gag gat tcc tac cgg aag cag gtg gtc att gat ggg Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly	35	40	45		144
gag acg tgc ctg ttg gac atc ctg gat acc gcc ggc cag gag gag tac Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr	50	55	60		192
agc gcc atg cgg gac cag tac atg cgc acc ggg gag ggc ttc ctg tgt Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys	65	70	75	80	240
gtg ttt gcc atc aac aac acc aag tct ttt gag gac atc cac cag tac Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr	85	90	95		288
agg gag cag atc aaa cgg gtg aag gac tcg gat gac gtg ccc atg gtg Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val	100	105	110		336
ctg gtg ggg aac aag tgt gac ctg gct gca cgc act gtg gaa tct cgg Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg	115	120	125		384
cag gct cag gac ctc gcc cga agc tac ggc atc ccc tac atc gag acc Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr	130	135	140		432
tcg gcc aag acc cgg cag gga gtg gag gat gcc ttc tac acg ttg gtg Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val	145	150	155	160	480
cgt gag atc cgg cag cac aag ctg cgg aag ctg aac cct cct gat gag Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu	165	170	175		528
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35 40 45
Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60
Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80
Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
85 90 95
Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
100 105 110
Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
115 120 125
Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
130 135 140
Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
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<210> 6
<211> 2004
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: fusion protein

<221> CDS

<222> (1) ... (2004)

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1 5 10 15

ttc aaa gat gcc gtg ttt gat ggc tcc agc tgc atc tct cct aca ata 96
Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
20 25 30

gtt cag cag ttt ggc tat cag cgc cg gca tca gat gat ggc aaa ctc 144
Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
35 40 45

aca gat cct tct aag aca agc aac act atc cgt gtt ttc ttg ccg aac 192
Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
50 55 60

aag caa aga aca gtc aat gtc cga aat gga atg agc ttg cat gac 240
Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
65 70 75 80

tgc ctt atg aaa gca ctc aag gtc agg ggc ctg caa cca gag tgc tgt 288
Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
85 90 95

gca gtg ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca cgc tta 336
Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
100 105 110

gat tgg aat act gat gct gcg tct ttg att gga gaa gaa ctt caa gta 384
Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
115 120 125

gat ttc ctg gat cat gtt ccc ctc aca aca cac aac ttt gct ccg aag 432
Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
130 135 140

acg ttc ctg aag ctt gcc ttc tgt gac atc tgt cag aaa ttc ctg ctc 480
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
145 150 155 160

aat gga ttt cga tgt cag act tgt ggc tac aaa ttt cat gag cac tgt 528
Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
165 170 175

agc acc aaa gta cct act atg tgt gtg gac tgg agt aac atc aga caa 576

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cont.

Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
180 185 190

ctc tta ttg ttt cca aat tcc act att ggt gat agt gga gtc cca gca 624
Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
195 200 205

cta cct tct ttg act atg cgt cgt atg cga gag tct gtt tcc agg atg 672
Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
210 215 220

cct gtt agt tct cag cac aga tat tct aca cct cac gcc ttc acc ttt 720
Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
225 230 235 240

aac acc tcc agt ccc tca tct gaa ggt tcc ctc tcc cag agg cag agg 768
Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
245 250 255

tcg aca tcc aca cct aat gtc cac atg gtc agc acc acg ctg cct gtg 816
Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
260 265 270

gac agc agg atg att gag gat gca att cga agt cac agc gaa tca gcc 864
Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
275 280 285

tca cct tca gcc ctg tcc agt agc ccc aac aat ctg agc cca aca ggc 912
Ser Pro Ser Ala Leu Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
290 295 300

tgg tca cag ccg aaa acc ccc gtg cca gca caa aga gag cgg gca cca 960
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305 310 315 320

gta tct ggg acc cag gag aaa aac aaa att agg cct cgt gga cag aga 1008
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
325 330 335

gat tca agc tat tat tgg gaa ata gaa gcc agt gaa gtg atg ctg tcc 1056
Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
340 345 350

act cgg att ggg tca ggc tct ttt gga act gtt tat aag ggt aaa tgg 1104
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
355 360 365

cac gga gat gtt gca gta aag atc cta aag gtt gtc gac cca acc cca 1152
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
370 375 380

gag caa ttc cag gcc ttc agg aat gag gtg gct gtt ctg cgc aaa aca 1200
Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr

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cg g cat gt g aac att ct g ctt ttc at g ggg tac at g aca aag gac aac				1248
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn				
405	410	415		
ct g gca att gt g acc cag tgg tgc gag ggc agc agc ctc tac aaa cac				1296
Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His				
420	425	430		
ct g cat gtc cag gag acc aag ttt cag at g ttc cag cta att gac att				1344
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile				
435	440	445		
gc c cg g cag ac g gct cag gga at g gac tat tt g cat gca aag aac at c				1392
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile				
450	455	460		
at c cat aga gac at g aaa tcc aac aat ata ttt ctc cat gaa ggc tta				1440
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu				
465	470	475	480	
ac a gt g aaa att gga gat ttt ggt tt g gca aca gta aag tca cgc tgg				1488
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp				
485	490	495		
ag t ggt tct cag cag gtt gaa caa cct act ggc tct gtc ctc tgg at g				1536
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met				
500	505	510		
gc c cca gag gt g atc cga at g cag gat aac aac cca ttc agt ttc cag				1584
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln				
515	520	525		
tc g gat gtc tac tcc tat ggc atc gta tt g tat gaa ct g at g ac g ggg				1632
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly				
530	535	540		
gag ctt cct tat tct cac atc aac aac cga gat cag atc atc ttc at g				1680
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met				
545	550	555	560	
gt g ggc cga gga tat gc c tcc cca gat ctt agt aag cta tat aag aac				1728
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn				
565	570	575		
tgc ccc aaa gca at g aag agg ct g gta gct gac tgt gt g aag aaa gta				1776
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val				
580	585	590		
aag gaa gag agg cct ctt ttt ccc cag atc ct g tct tcc att gag ct g				1824
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu				
595	600	605		

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a
Cont.

ctc caa cac tct cta ccg aag atc aac cg^g agc gct tcc gag cca tcc 1872
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
610 615 620

ttg cat cg^g gca gcc cac act gag gat atc aat gct tgc acg ctg acc 1920
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
625 630 635 640

acg tcc ccg agg ctg cct gtc ttc tac tcg ttc ctg ccg ttc ttc ttc 1968
Thr Ser Pro Arg Leu Pro Val Phe Tyr Ser Phe Leu Pro Phe Phe Phe
645 650 655

ttc ttc ttc tcg ttc tgt ttc acg cct agt aca ttc 2004
Phe Phe Phe Ser Phe Cys Phe Thr Pro Ser Thr Phe
660 665

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<211> 668
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: fusion protein

<400> 7

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Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
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Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
35 40 45
Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
50 55 60
Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
65 70 75 80
Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
85 90 95
Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
100 105 110
Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
115 120 125
Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
130 135 140
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
145 150 155 160
Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
165 170 175
Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
180 185 190
Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
195 200 205

*A
Cont.*

Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
210 215 220
Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
225 230 235 240
Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
245 250 255
Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
260 265 270
Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
275 280 285
Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
290 295 300
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305 310 315 320
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
325 330 335
Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
340 345 350
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
355 360 365
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
370 375 380
Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
385 390 395 400
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
405 410 415
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420 425 430
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
435 440 445
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
450 455 460
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
465 470 475 480
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
485 490 495
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
500 505 510
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
515 520 525
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
530 535 540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545 550 555 560
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
565 570 575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
580 585 590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
595 600 605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
610 615 620
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr

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Cont.

625 630 635 640
Thr Ser Pro Arg Leu Pro Val Phe Tyr Ser Phe Leu Pro Phe Phe Phe
645 650 655
Phe Phe Phe Ser Phe Cys Phe Thr Pro Ser Thr Phe
660 665

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